

FIGURE 2

MVRKNPPLRNVASEGEGQILEPIGTESKVSIGNKEFSADQMSEN TDQSDAAELNHKEEHLHVQDPSSSSKKDLKSAVLSEKAGFN YE
SPSKGNGFPSPHDEVTDRNMLAFSFPAAAGVCEPLKSPQRAEADDPQDMACTPSGDSLETKEQKMSPKATEETGQAQSGQANCQGLS
PVSVASKNPQVPSDGGVRLNKSCTDLLVNDNPDPAPLSPELQDFKCNICGYGYGNDPTDLIKHFRKYHLGLHNRTRQDAELDSKILAL
HNMVQFSHSDQFQKVNRSVFSGLQDINSSRPVLLNGTYDVQVTSGGTFIGIGRKTDDCQGN TKYFRCKFCNF TYMGNSSTELEQHFLQ
THPNKIKASLPSSEVAKPSEKNSNKSIPALQSSDSGDLGKWQDKITVKAGDDTPVGYSVPIKPLDSSRQNGTEATSYIWCCKFCSPSCES
SSSLKLEHYGKQHGAVQSGGLNPELNDKLSRGSVINQNDLAKSSEGETMTKTDKSSSGAKKKDFSSKGAEDNMVTSYNCQFCDFRYSK
SHGPDVIVVGPLLRHYQQHLNHHKCTIKHCPFCPRGLCSPEKHLGEITYPFACRKSNCSCALLLHLSPGAAGSSRVKHQCHQCSFTT
PDVDVLLFHYESVHESQASDVKQEANHLQSGDQQSVKESKEHSC TKCDFITQVEEII SRHYRRAHSCYKCRQCSFTAADTQSLLEHFN
TVHCQEQDIT TANGEEDGHAISTIKKEPKIDFRVYNLLTPDSKMGEPSVESVVKREKLEEKDGLKEKVWTESSSDDLNRNVTRGADILR
GSPSYTQASLGLLTPVSGTQEQT KTLRDSPNVEAAHLARPIYGLAVETKGFLQGAPAGGEKSGALPQQYPASGENKSKDESQSLLRRRR
GSGVFCANCLTTKTSLRKNANGGYVCNACGLYQKLHSTPRPLNI I KQNGEQI I RRRTRKRLNPEALQAEQLNKQQRGSNEEQVNGSP
LERRSEDHLTESHQREI PLPSLSKYEAQGS LTKSHSAQQPVLVSQTLDIHKRMQPLHIQIKSPQESTGDPGNSSSVSEGGSSSERGSP I
EKYMRPAKHPNYSPPGSP I EKYQYPLFGLPFVHNDFQSEADWLRFWSKYKLSVPGNPHYLSHVPGLPNPCQNYVPYPTFNLPPHFSAVG
SDNDIPLDLAIKHSRPGPTANGASKEKT KAPPNVKNEGPLNVVKT EKVDRSTQDELSTKCVHCIGIVFLDEVMYALHMSCHGDSGPGFQCS
ICQHLCTDKYDFTTHIQRGLHRNNAQVEKNGKPK E

FIGURE 3A

original BCY1	(1)	1	111
MC50A19 BCY I	(1)	---	GCCGAGCTGCGCTGAAGGGCAGCAGCAACACCGAGAGTGTGTTCCCGTGCCCACTCCGAGCACGTGGCCCGAGATCGTGGGCGAGGCAAGGCTGCAAGATTAAAGGC
MC50A6 BCY I	(1)	ATGGCCGAGCTGCGCTGAAGGGCGGCGAGCAACACCGAGTGTGTTCCCGTGCCCACTCCGAGCACGTGGCCCGAGATCGTGGGCGAGGCAAGGCTGCAAGATTAAAGGC	
MC50A8 BCY I	(1)	ATGGCCGAGCTGCGCTGAAGGGCGGCGAGCAACACCGAGTGTGTTCCCGTGCCCACTCCGAGCACGTGGCCCGAGATCGTGGGCGAGGCAAGGCTGCAAGATTAAAGGC	
MC54..21 BCY I	(1)	ATGGCCGAGCTGCGCTGAAGGGCGGCGAGCAACACCGAGTGTGTTCCCGTGCCCACTCCGAGCACGTGGCCCGAGATCGTGGGCGAGGCAAGGCTGCAAGATTAAAGGC	
MC55..29 BCY I	(1)	ATGGCCGAGCTGCGCTGAAGGGCGGCGAGCAACACCGAGTGTGTTCCCGTGCCCACTCCGAGCACGTGGCCCGAGATCGTGGGCGAGGCAAGGCTGCAAGATTAAAGGC	
MC55..32 BCY I	(1)	ATGGCCGAGCTGCGCTGAAGGGCGGCGAGCAACACCGAGTGTGTTCCCGTGCCCACTCCGAGCACGTGGCCCGAGATCGTGGGCGAGGCAAGGCTGCAAGATTAAAGGC	
Consensus	(1)	111	ATGGCCGAGCTGCGCTGAAGGGCGGCGAGCAACACCGAGTGTGTTCCCGTGCCCACTCCGAGCACGTGGCCCGAGATCGTGGGCGAGGCAAGGCTGCAAGATTAAAGGC
original BCY1	(108)	111	
MC50A19 BCY I	(111)	CTTGAGGGCCAGACCAACCTACATCAAGACACCGGTGAGGGGCGAGGAACCAAGTGTTCATGTGTGACAGGGCGACGGGAGGACGTGGCCACACAGCCCCGGGAAATCA	
MC50A6 BCY I	(111)	CTTGAGGGCCAGACCAACCTACATCAAGACACCGGTGAGGGGCGAGGAACCAAGTGTTCATGTGTGACAGGGCGACGGGAGGACGTGGCCACACAGCCCCGGGAAATCA	
MC50A8 BCY I	(111)	CTTGAGGGCCAGACCAACCTACATCAAGACACCGGTGAGGGGCGAGGAACCAAGTGTTCATGTGTGACAGGGCGACGGGAGGACGTGGCCACACAGCCCCGGGAAATCA	
MC54..21 BCY I	(111)	CTTGAGGGCCAGACCAACCTACATCAAGACACCGGTGAGGGGCGAGGAACCAAGTGTTCATGTGTGACAGGGCGACGGGAGGACGTGGCCACACAGCCCCGGGAAATCA	
MC55..29 BCY I	(111)	CTTGAGGGCCAGACCAACCTACATCAAGACACCGGTGAGGGGCGAGGAACCAAGTGTTCATGTGTGACAGGGCGACGGGAGGACGTGGCCACACAGCCCCGGGAAATCA	
MC55..32 BCY I	(111)	CTTGAGGGCCAGACCAACCTACATCAAGACACCGGTGAGGGGCGAGGAACCAAGTGTTCATGTGTGACAGGGCGACGGGAGGACGTGGCCACACAGCCCCGGGAAATCA	
Consensus	(111)	221	CTTGAGGGCCAGACCAACCTACATCAAGACACCGGTGAGGGGCGAGGAACCAAGTGTTCATGTGTGACAGGGCGACGGGAGGACGTGGCCACACAGCCCCGGGAAATCA
original BCY1	(218)	221	
MC50A19 BCY I	(221)	TCTCAGCAGCGGAGCACTTCTCCATGATCCGTGCTCCCGCAACAAGTCAGGCGCCGCTTTGGTGTGGCTCCTGTCTGCTCCGCGCCAGGTGACCATCCGTGTGCGGGTG	
MC50A6 BCY I	(221)	TCTCAGCAGCGGAGCACTTCTCCATGATCCGTGCTCCCGCAACAAGTCAGGCGCCGCTTTGGTGTGGCTCCTGTCTGCTCCGCGCCAGGTGACCATCCGTGTGCGGGTG	
MC50A8 BCY I	(221)	TCTCAGCAGCGGAGCACTTCTCCATGATCCGTGCTCCCGCAACAAGTCAGGCGCCGCTTTGGTGTGGCTCCTGTCTGCTCCGCGCCAGGTGACCATCCGTGTGCGGGTG	
MC54..21 BCY I	(221)	TCTCAGCAGCGGAGCACTTCTCCATGATCCGTGCTCCCGCAACAAGTCAGGCGCCGCTTTGGTGTGGCTCCTGTCTGCTCCGCGCCAGGTGACCATCCGTGTGCGGGTG	
MC55..29 BCY I	(221)	TCTCAGCAGCGGAGCACTTCTCCATGATCCGTGCTCCCGCAACAAGTCAGGCGCCGCTTTGGTGTGGCTCCTGTCTGCTCCGCGCCAGGTGACCATCCGTGTGCGGGTG	
MC55..32 BCY I	(221)	TCTCAGCAGCGGAGCACTTCTCCATGATCCGTGCTCCCGCAACAAGTCAGGCGCCGCTTTGGTGTGGCTCCTGTCTGCTCCGCGCCAGGTGACCATCCGTGTGCGGGTG	
Consensus	(221)	330	TCTCAGCAGCGGAGCACTTCTCCATGATCCGTGCTCCCGCAACAAGTCAGGCGCCGCTTTGGTGTGGCTCCTGTCTGCTCCGCGCCAGGTGACCATCCGTGTGCGGGTG
original BCY1	(328)	331	
MC50A19 BCY I	(331)	CCCTACCGCGTGGTGGGCTGGTGGGCCCCAAAGGGGCAACCATCAAGCGCATCCAGCAGCAACCAACACATACATTATCAACCAAGCGGTGACCGCGACCCCGT	
MC50A6 BCY I	(331)	CCCTACCGCGTGGTGGGCTGGTGGGCCCCAAAGGGGCAACCATCAAGCGCATCCAGCAGCAACCAACACATATATCAACCAAGCGGTGACCGCGACCCCGT	
MC50A8 BCY I	(331)	CCCTACCGCGTGGTGGGCTGGTGGGCCCCAAAGGGGCAACCATCAAGCGCATCCAGCAGCAACCAACACATATATCAACCAAGCGGTGACCGCGACCCCGT	
MC54..21 BCY I	(331)	CCCTACCGCGTGGTGGGCTGGTGGGCCCCAAAGGGGCAACCATCAAGCGCATCCAGCAGCAACCAACACATATATCAACCAAGCGGTGACCGCGACCCCGT	
MC55..29 BCY I	(331)	CCCTACCGCGTGGTGGGCTGGTGGGCCCCAAAGGGGCAACCATCAAGCGCATCCAGCAGCAACCAACACATATATCAACCAAGCGGTGACCGCGACCCCGT	
MC55..32 BCY I	(331)	CCCTACCGCGTGGTGGGCTGGTGGGCCCCAAAGGGGCAACCATCAAGCGCATCCAGCAGCAACCAACACATATATCAACCAAGCGGTGACCGCGACCCCGT	
Consensus	(331)	440	CCCTACCGCGTGGTGGGCTGGTGGGCCCCAAAGGGGCAACCATCAAGCGCATCCAGCAGCAACCAACACATATATCAACCAAGCGGTGACCGCGACCCCGT

FIGURE 3A

original BCY1	441	GTTCGAGATCACGGGTGCCCCAGGCAACGCTGGAGCGTGGCGGAGGAGATCGAGACGCACATCGCGGTGGCACTGGCAAGATCCTCGAGTACAACAATGAAAAACGACT	550
MC50A19 BCY I	(438)	GTTCGAGATCACGGGTGCCCCAGGCAACGCTGGAGCGTGGCGGAGGAGATCGAGACGCACATCGCGGTGGCACTGGCAAGATCCTCGAGTACAACAATGAAAAACGACT	
MC50A6 BCY I	(441)	GTTCGAGATCACGGGTGCCCCAGGCAACGCTGGAGCGTGGCGGAGGAGATCGAGACGCACATCGCGGTGGCACTGGCAAGATCCTCGAGTACAACAATGAAAAACGACT	
MC50A8 BCY I	(441)	GTTCGAGATCACGGGTGCCCCAGGCAACGCTGGAGCGTGGCGGAGGAGATCGAGACGCACATCGCGGTGGCACTGGCAAGATCCTCGAGTACAACAATGAAAAACGACT	
MC54.21 BCY I	(441)	GTTCGAGATCACGGGTGCCCCAGGCAACGCTGGAGCGTGGCGGAGGAGATCGAGACGCACATCGCGGTGGCACTGGCAAGATCCTCGAGTACAACAATGAAAAACGACT	
MC55.29 BCY I	(441)	GTTCGAGATCACGGGTGCCCCAGGCAACGCTGGAGCGTGGCGGAGGAGATCGAGACGCACATCGCGGTGGCACTGGCAAGATCCTCGAGTACAACAATGAAAAACGACT	
MC55.32 BCY I	(441)	GTTCGAGATCACGGGTGCCCCAGGCAACGCTGGAGCGTGGCGGAGGAGATCGAGACGCACATCGCGGTGGCACTGGCAAGATCCTCGAGTACAACAATGAAAAACGACT	
Consensus		GTTCGAGATCACGGGTGCCCCAGGCAACGCTGGAGCGTGGCGGAGGAGATCGAGACGCACATCGCGGTGGCACTGGCAAGATCCTCGAGTACAACAATGAAAAACGACT	
original BCY1	551	TCCTGGCGGGAGCCCGACGACGAGCAATCGATAGCCGCTACTCCGACGCCCTGGCGGGTGCAACGACCCGCTTCCACCTTCGCGGACAGACAGCCTGGGC	660
MC50A19 BCY I	(548)	TCCTGGCGGGAGCCCGACGACGAGCAATCGATAGCCGCTACTCCGACGCCCTGGCGGGTGCAACGACCCGCTTCCACCTTCGCGGACAGACAGCCTGGGC	
MC50A6 BCY I	(551)	TCCTGGCGGGAGCCCGACGACGAGCAATCGATAGCCGCTACTCCGACGCCCTGGCGGGTGCAACGACCCGCTTCCACCTTCGCGGACAGACAGCCTGGGC	
MC50A8 BCY I	(551)	TCCTGGCGGGAGCCCGACGACGAGCAATCGATAGCCGCTACTCCGACGCCCTGGCGGGTGCAACGACCCGCTTCCACCTTCGCGGACAGACAGCCTGGGC	
MC54.21 BCY I	(551)	TCCTGGCGGGAGCCCGACGACGAGCAATCGATAGCCGCTACTCCGACGCCCTGGCGGGTGCAACGACCCGCTTCCACCTTCGCGGACAGACAGCCTGGGC	
MC55.29 BCY I	(551)	TCCTGGCGGGAGCCCGACGACGAGCAATCGATAGCCGCTACTCCGACGCCCTGGCGGGTGCAACGACCCGCTTCCACCTTCGCGGACAGACAGCCTGGGC	
MC55.32 BCY I	(551)	TCCTGGCGGGAGCCCGACGACGAGCAATCGATAGCCGCTACTCCGACGCCCTGGCGGGTGCAACGACCCGCTTCCACCTTCGCGGACAGACAGCCTGGGC	
Consensus		TCCTGGCGGGAGCCCGACGACGAGCAATCGATAGCCGCTACTCCGACGCCCTGGCGGGTGCAACGACCCGCTTCCACCTTCGCGGACAGACAGCCTGGGC	
original BCY1	661	TGCATCGGCGAGTGGGAGTGGAATCTGGCTTTGAGGCCCCACGCCCTGGGTGAGCAGGGCGGGGACTTTGGCTACGGCGGGTACCTCTTTCGCGGCTATGGCGTGGGCAA	770
MC50A19 BCY I	(658)	TGCATCGGCGAGTGGGAGTGGAATCTGGCTTTGAGGCCCCACGCCCTGGGTGAGCAGGGCGGGGACTTTGGCTACGGCGGGTACCTCTTTCGCGGCTATGGCGTGGGCAA	
MC50A6 BCY I	(661)	TGCATCGGCGAGTGGGAGTGGAATCTGGCTTTGAGGCCCCACGCCCTGGGTGAGCAGGGCGGGGACTTTGGCTACGGCGGGTACCTCTTTCGCGGCTATGGCGTGGGCAA	
MC50A8 BCY I	(661)	TGCATCGGCGAGTGGGAGTGGAATCTGGCTTTGAGGCCCCACGCCCTGGGTGAGCAGGGCGGGGACTTTGGCTACGGCGGGTACCTCTTTCGCGGCTATGGCGTGGGCAA	
MC54.21 BCY I	(661)	TGCATCGGCGAGTGGGAGTGGAATCTGGCTTTGAGGCCCCACGCCCTGGGTGAGCAGGGCGGGGACTTTGGCTACGGCGGGTACCTCTTTCGCGGCTATGGCGTGGGCAA	
MC55.29 BCY I	(661)	TGCATCGGCGAGTGGGAGTGGAATCTGGCTTTGAGGCCCCACGCCCTGGGTGAGCAGGGCGGGGACTTTGGCTACGGCGGGTACCTCTTTCGCGGCTATGGCGTGGGCAA	
MC55.32 BCY I	(661)	TGCATCGGCGAGTGGGAGTGGAATCTGGCTTTGAGGCCCCACGCCCTGGGTGAGCAGGGCGGGGACTTTGGCTACGGCGGGTACCTCTTTCGCGGCTATGGCGTGGGCAA	
Consensus		TGCATCGGCGAGTGGGAGTGGAATCTGGCTTTGAGGCCCCACGCCCTGGGTGAGCAGGGCGGGGACTTTGGCTACGGCGGGTACCTCTTTCGCGGCTATGGCGTGGGCAA	
original BCY1	771	GCAGGATGTGTACTACGGCGTGGCCGAGACTAGCCCCCGCTGTGGCGGGCCAGGAGAACGCCACGCCACCTCCGTGCTCTTCTCCTCCTCCTCCTCCT	880
MC50A19 BCY I	(768)	GCAGGATGTGTACTACGGCGTGGCCGAGACTAGCCCCCGCTGTGGCGGGCCAGGAGAACGCCACGCCACCTCCGTGCTCTTCTCCTCCTCCTCCTCCT	
MC50A6 BCY I	(771)	GCAGGATGTGTACTACGGCGTGGCCGAGACTAGCCCCCGCTGTGGCGGGCCAGGAGAACGCCACGCCACCTCCGTGCTCTTCTCCTCCTCCTCCTCCT	
MC50A8 BCY I	(771)	GCAGGATGTGTACTACGGCGTGGCCGAGACTAGCCCCCGCTGTGGCGGGCCAGGAGAACGCCACGCCACCTCCGTGCTCTTCTCCTCCTCCTCCTCCT	
MC54.21 BCY I	(771)	GCAGGATGTGTACTACGGCGTGGCCGAGACTAGCCCCCGCTGTGGCGGGCCAGGAGAACGCCACGCCACCTCCGTGCTCTTCTCCTCCTCCTCCTCCT	
MC55.29 BCY I	(771)	GCAGGATGTGTACTACGGCGTGGCCGAGACTAGCCCCCGCTGTGGCGGGCCAGGAGAACGCCACGCCACCTCCGTGCTCTTCTCCTCCTCCTCCTCCT	
MC55.32 BCY I	(771)	GCAGGATGTGTACTACGGCGTGGCCGAGACTAGCCCCCGCTGTGGCGGGCCAGGAGAACGCCACGCCACCTCCGTGCTCTTCTCCTCCTCCTCCTCCT	
Consensus		GCAGGATGTGTACTACGGCGTGGCCGAGACTAGCCCCCGCTGTGGCGGGCCAGGAGAACGCCACGCCACCTCCGTGCTCTTCTCCTCCTCCTCCTCCT	

FIGURE 3A

original BCY1	(878)	881	CTTCCGCCAAGGCCCGCGCTGGGCCCCCGGGCGGCAACCGCTCCCTGTCACATTCCGGGACCCGAGCTGCCCGGACTCCCGAGCGCCCCCGGGAGAGCCGCTCCRG	990
MC50A19 BCY I	(881)		CTTCCGCCAAGGCCCGCGCTGGGCCCCCGGGCGGCAACCGCTCCCTGTCACATTCCGGGACCCGAGCTGCCCGGACTCCCGAGCGCCCCCGGGAGAGCCGCTCCAG	
MC50A6 BCY I	(881)		CTTCCGCCAAGGCCCGCGCTGGGCCCCCGGGCGGCAACCGCTCCCTGTCACATTCCGGGACCCGAGCTGCCCGGACTCCCGAGCGCCCCCGGGAGAGCCGCTCCAG	
MC50A8 BCY I	(881)		CTTCCGCCAAGGCCCGCGCTGGGCCCCCGGGCGGCAACCGCTCCCTGTCACATTCCGGGACCCGAGCTGCCCGGACTCCCGAGCGCCCCCGGGAGAGCCGCTCCAG	
MC54.21 BCY I	(881)		CTTCCGCCAAGGCCCGCGCTGGGCCCCCGGGCGGCAACCGCTCCCTGTCACATTCCGGGACCCGAGCTGCCCGGACTCCCGAGCGCCCCCGGGAGAGCCGCTCCAG	
MC55.29 BCY I	(881)		CTTCCGCCAAGGCCCGCGCTGGGCCCCCGGGCGGCAACCGCTCCCTGTCACATTCCGGGACCCGAGCTGCCCGGACTCCCGAGCGCCCCCGGGAGAGCCGCTCCAG	
MC55.32 BCY I	(881)		CTTCCGCCAAGGCCCGCGCTGGGCCCCCGGGCGGCAACCGCTCCCTGTCACATTCCGGGACCCGAGCTGCCCGGACTCCCGAGCGCCCCCGGGAGAGCCGCTCCAG	
Consensus			991	
original BCY1	(988)		GGCTTCTCTAAACTTGGTGGGGCGGCTGCGAGCCCCGAGCGCGGGGATTGCATGGTCTGCTTTGAGAGCGAAGTGACTGCCGCCCTTGTGCCCCCTGCGGACA	1100
MC50A19 BCY I	(991)		GGCTTCTCTAAACTTGGTGGGGCGGCTGCGAGCCCCGAGCGCGGGGATTGCATGGTCTGCTTTGAGAGCGAAGTGACTGCCGCCCTTGTGCCCCCTGCGGACA	
MC50A6 BCY I	(991)		GGCTTCTCTAAACTTGGTGGGGCGGCTGCGAGCCCCGAGCGCGGGGATTGCATGGTCTGCTTTGAGAGCGAAGTGACTGCCGCCCTTGTGCCCCCTGCGGACA	
MC50A8 BCY I	(991)		GGCTTCTCTAAACTTGGTGGGGCGGCTGCGAGCCCCGAGCGCGGGGATTGCATGGTCTGCTTTGAGAGCGAAGTGACTGCCGCCCTTGTGCCCCCTGCGGACA	
MC54.21 BCY I	(991)		GGCTTCTCTAAACTTGGTGGGGCGGCTGCGAGCCCCGAGCGCGGGGATTGCATGGTCTGCTTTGAGAGCGAAGTGACTGCCGCCCTTGTGCCCCCTGCGGACA	
MC55.29 BCY I	(991)		GGCTTCTCTAAACTTGGTGGGGCGGCTGCGAGCCCCGAGCGCGGGGATTGCATGGTCTGCTTTGAGAGCGAAGTGACTGCCGCCCTTGTGCCCCCTGCGGACA	
MC55.32 BCY I	(991)		GGCTTCTCTAAACTTGGTGGGGCGGCTGCGAGCCCCGAGCGCGGGGATTGCATGGTCTGCTTTGAGAGCGAAGTGACTGCCGCCCTTGTGCCCCCTGCGGACA	
Consensus			1101	
original BCY1	(1098)		CAACCTGTTCTGCATGGAGTGTGCAGTACGCATCTGCGAGAGGACGGACCCAGAGTGTCCCCGTCTGCCCATCACAGCCACGCAAGCCATCCGAATATTCTCCTAA	1210
MC50A19 BCY I	(1098)		CAACCTGTTCTGCATGGAGTGTGCAGTACGCATCTGCGAGAGGACGGACCCAGAGTGTCCCCGTCTGCCCATCACAGCCGCGCAAGCCATCCGAATATTCTCCTAAGGAT	
MC50A6 BCY I	(1098)		CAACCTGTTCTGCATGGAGTGTGCAGTACGCATCTGCGAGAGGACGGACCCAGAGTGTCCCCGTCTGCCCATCACAGCCGCGCAAGCCATCCGAATATTCTCCTAAGGAT	
MC50A8 BCY I	(1098)		CAACCTGTTCTGCATGGAGTGTGCAGTACGCATCTGCGAGAGGACGGACCCAGAGTGTCCCCGTCTGCCCATCACAGCCGCGCAAGCCATCCGAATATTCTCCTAAGGAT	
MC54.21 BCY I	(1098)		CAACCTGTTCTGCATGGAGTGTGCAGTACGCATCTGCGAGAGGACGGACCCAGAGTGTCCCCGTCTGCCCATCACAGCCGCGCAAGCCATCCGAATATTCTCCTAAGGAT	
MC55.29 BCY I	(1098)		CAACCTGTTCTGCATGGAGTGTGCAGTACGCATCTGCGAGAGGACGGACCCAGAGTGTCCCCGTCTGCCCATCACAGCCGCGCAAGCCATCCGAATATTCTCCTAAGGAT	
MC55.32 BCY I	(1098)		CAACCTGTTCTGCATGGAGTGTGCAGTACGCATCTGCGAGAGGACGGACCCAGAGTGTCCCCGTCTGCCCATCACAGCCGCGCAAGCCATCCGAATATTCTCCTAAGGAT	
Consensus	(1101)		1211	
original BCY1	(1204)		-----	1248
MC50A19 BCY I	(1208)		CCACTAGTCCAGTGTGGGAATTCTGCAGATATCCA	
MC50A6 BCY I	(1208)		CCACTAGTCCAGTGTGGGAATTCTGCAGATATCCA	
MC50A8 BCY I	(1208)		CCACTAGTCCAGTGTGGGAATTCTGCAGATATCCA	
MC54.21 BCY I	(1204)		-----	
MC55.29 BCY I	(1204)		-----	
MC55.32 BCY I	(1204)		-----	
Consensus	(1211)		-----	

FIGURE 3B

MAELRLKGSS NTTECVPVPT SEHVAEIVGR QGCKIKALRA KNTYIKTPV RGEFPVFMVT GRREDVATAR REIISAAEHF SMIRASRNKS
GAAFGVAPAL PGQVTIRVRV PYRVVGLVVG PKGATIKRIQ QQTNTYIITP SRDRDPVFEI TGAPGNVERA REEETHIAV RTGKILEYNN
ENDFLAGSPD AAIDSRYSDA WRVHQPGCKP LSTFRQNSLG CIGECGVDSG FEAPRLGEQG GDFGYGGYLF PGYGVGKQDV YYGVAETSPP
LWAGQENATP TSVLFSSASS SSSSSAKARA GPPGAHRSPA TSAGPELAGL PRRPGEPLQ GFSLGGGGL RSPGGGRDCM VCFESEVTAA
LVPCGHNLCF MECAVRICER TDPECPVCHI TAAQAIRIFS

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